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Sequence Listing could not be accepted due to errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866)
217-9197 (toll free).

Reviewer: Keisha Douglas

Timestamp: [year=2009; month=1; day=22; hr=12; min=45; sec=12; ms=146;]

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Reviewer Comments:

Leu Glu Phe
30

Tyr Thr Lys Arg Leu Phe Gln Ser Val Ser Pro Ser Phe Leu Ser Ile
35 40 45

Please correct invalid amino acid numbering shown above in sequence id#
48. Please check the remaining sequences for similar errors.

Application No: 10785116 Version No: 3.0

Input Set:

Output Set:

Started: 2009-01-07 15:10:48.392
Finished: 2009-01-07 15:10:52.884
Elapsed: 0 hr(s) 0 min(s) 4 sec(s) 492 ms
Total Warnings: 33
Total Errors: 9
No. of SeqIDs Defined: 49
Actual SeqID Count: 49

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (1)
W 213	Artificial or Unknown found in <213> in SEQ ID (2)
W 213	Artificial or Unknown found in <213> in SEQ ID (3)
W 213	Artificial or Unknown found in <213> in SEQ ID (4)
W 213	Artificial or Unknown found in <213> in SEQ ID (5)
W 213	Artificial or Unknown found in <213> in SEQ ID (6)
W 213	Artificial or Unknown found in <213> in SEQ ID (7)
W 213	Artificial or Unknown found in <213> in SEQ ID (8)
E 201	Mandatory field data missing in <223> in SEQ ID (11)
E 201	Mandatory field data missing in <223> in SEQ ID (15)
W 213	Artificial or Unknown found in <213> in SEQ ID (17)
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W 213	Artificial or Unknown found in <213> in SEQ ID (20)
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W 213	Artificial or Unknown found in <213> in SEQ ID (22)
W 213	Artificial or Unknown found in <213> in SEQ ID (23)
W 213	Artificial or Unknown found in <213> in SEQ ID (24)
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Input Set:

Output Set:

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Actual SeqID Count: 49

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (27)
W 213	Artificial or Unknown found in <213> in SEQ ID (28) This error has occurred more than 20 times, will not be displayed
E 201	Mandatory field data missing in <223> in SEQ ID (45)
E 323	Invalid/missing amino acid numbering SEQID (48)at Protein (35)
E 323	Invalid/missing amino acid numbering SEQID (48) POS (36)
E 323	Invalid/missing amino acid numbering SEQID (48)at Protein (40)
E 323	Invalid/missing amino acid numbering SEQID (48) POS (41)
E 323	Invalid/missing amino acid numbering SEQID (48)at Protein (45)
E 323	Invalid/missing amino acid numbering SEQID (48) POS (46)

SEQUENCE LISTING

<110> Pecker, Iris
Vlodavsky , Israel
Feinstein, Elena

<120> POLYNUCLEOTIDE ENCODING A POLYPEPTIDE HAVING HEPARANASE ACTIVITY AND EXPRESSION OF SAME
IN GENETICALLY MODIFIED CELLS

<130> 27674

<140> 10785116

<141> 2004-02-25

<160> 49

<170> PatentIn version 3.1

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<213> Artificial sequence

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<223> Synthetic oligonucleotide

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<211> 24

<212> DNA

<213> Artificial sequence

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<223> Synthetic oligonucleotide

<400> 2

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<210> 3

<211> 23

<212> DNA

<213> Artificial sequence

<220>

<223> Synthetic oligonucleotide

<400> 3

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<210> 4

<211> 22

<212> DNA

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<223> Synthetic oligonucleotide

<400> 4

gcacatttagc cgtctttctt cg 22

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<212> DNA

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<223> Synthetic oligonucleotide

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<211> 23

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<223> Synthetic oligonucleotide

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<211> 24

<212> DNA

<213> Artificial sequence

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<223> Synthetic oligonucleotide

<400> 7

gtagtgatgc catgtaactg aatc 24

<210> 8

<211> 9

<212> PRT

<213> Artificial sequence

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<223> Peptide derived from tryptic digestion of human heparinase

<400> 8

Tyr Gly Pro Asp Val Gly Gln Pro Arg

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<212> DNA
<213> Homo sapiens

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 <211> 543
 <212> PRT
 <213> Homo sapiens

<400> 10

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 20 25 30

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 35 40 45

Leu His Leu Val Ser Pro Ser Phe Leu Ser Val Thr Ile Asp Ala Asn
 50 55 60

Leu Ala Thr Asp Pro Arg Phe Leu Ile Leu Leu Gly Ser Pro Lys Leu
 65 70 75 80

Arg Thr Leu Ala Arg Gly Leu Ser Pro Ala Tyr Leu Arg Phe Gly Gly
 85 90 95

Thr Lys Thr Asp Phe Leu Ile Phe Asp Pro Lys Lys Glu Ser Thr Phe
 100 105 110

Glu Glu Arg Ser Tyr Trp Gln Ser Gln Val Asn Gln Asp Ile Cys Lys
 115 120 125

Tyr Gly Ser Ile Pro Pro Asp Val Glu Glu Lys Leu Arg Leu Glu Trp
 130 135 140

Pro Tyr Gln Glu Gln Leu Leu Leu Arg Glu His Tyr Gln Lys Lys Phe
 145 150 155 160

Lys	Asn	Ser	Thr	Tyr	Ser	Arg	Ser	Ser	Val	Asp	Val	Leu	Tyr	Thr	Phe	165	170	175	
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Arg	Thr	Ala	Asp	Leu	Gln	Trp	Asn	Ser	Ser	Asn	Ala	Gln	Leu	Leu	Leu	195	200	205	
Asp	Tyr	Cys	Ser	Ser	Lys	Gly	Tyr	Asn	Ile	Ser	Trp	Glu	Leu	Gly	Asn	210	215	220	
Glu	Pro	Asn	Ser	Phe	Leu	Lys	Lys	Ala	Asp	Ile	Phe	Ile	Asn	Gly	Ser	225	230	235	240
Gln	Leu	Gly	Glu	Asp	Tyr	Ile	Gln	Leu	His	Lys	Leu	Leu	Arg	Lys	Ser	245	250	255	
Thr	Phe	Lys	Asn	Ala	Lys	Leu	Tyr	Gly	Pro	Asp	Val	Gly	Gln	Pro	Arg	260	265	270	
Arg	Lys	Thr	Ala	Lys	Met	Leu	Lys	Ser	Phe	Leu	Lys	Ala	Gly	Gly	Glu	275	280	285	
Val	Ile	Asp	Ser	Val	Thr	Trp	His	His	Tyr	Tyr	Leu	Asn	Gly	Arg	Thr	290	295	300	
Ala	Thr	Arg	Glu	Asp	Phe	Leu	Asn	Pro	Asp	Val	Leu	Asp	Ile	Phe	Ile	305	310	315	320
Ser	Ser	Val	Gln	Lys	Val	Phe	Gln	Val	Val	Glu	Ser	Thr	Arg	Pro	Gly	325	330	335	
Lys	Lys	Val	Trp	Leu	Gly	Glu	Thr	Ser	Ser	Ala	Tyr	Gly	Gly	Gly	Ala	340	345	350	
Pro	Leu	Leu	Ser	Asp	Thr	Phe	Ala	Ala	Gly	Phe	Met	Trp	Leu	Asp	Lys	355	360	365	
Leu	Gly	Leu	Ser	Ala	Arg	Met	Gly	Ile	Glu	Val	Val	Met	Arg	Gln	Val	370	375	380	

Phe Phe Gly Ala Gly Asn Tyr His Leu Val Asp Glu Asn Phe Asp Pro
 385 390 395 400

Leu Pro Asp Tyr Trp Leu Ser Leu Leu Phe Lys Lys Leu Val Gly Thr
 405 410 415

Lys Val Leu Met Ala Ser Val Gln Gly Ser Lys Arg Arg Lys Leu Arg
 420 425 430

Val Tyr Leu His Cys Thr Asn Thr Asp Asn Pro Arg Tyr Lys Glu Gly
 435 440 445

Asp Leu Thr Leu Tyr Ala Ile Asn Leu His Asn Val Thr Lys Tyr Leu
 450 455 460

Arg Leu Pro Tyr Pro Phe Ser Asn Lys Gln Val Asp Lys Tyr Leu Leu
 465 470 475 480

Arg Pro Leu Gly Pro His Gly Leu Leu Ser Lys Ser Val Gln Leu Asn
 485 490 495

Gly Leu Thr Leu Lys Met Val Asp Asp Gln Thr Leu Pro Pro Leu Met
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Glu Lys Pro Leu Arg Pro Gly Ser Ser Leu Gly Leu Pro Ala Phe Ser
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Tyr Ser Phe Phe Val Ile Arg Asn Ala Lys Val Ala Ala Cys Ile
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 <213> Homo sapiens

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 <221> CDS
 <222> (63)..(1691)
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 Met Leu Leu Arg Ser Lys Pro Ala Leu Pro Pro Pro Leu Met Leu

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ctg ctc ctg ggg ccg ctg ggt ccc ctc tcc cct ggc gcc ctg ccc cga				155
Leu Leu Leu Gly Pro Leu Gly Pro Leu Ser Pro Gly Ala Leu Pro Arg				
	20	25	30	
cct gcg caa gca cag gac gtc gtg gac ctg gac ttc ttc acc cag gag				203
Pro Ala Gln Ala Gln Asp Val Val Asp Leu Asp Phe Phe Thr Gln Glu				
	35	40	45	
ccg ctg cac ctg gtg agc ccc tcg ttc ctg tcc gtc acc att gac gcc				251
Pro Leu His Leu Val Ser Pro Ser Phe Leu Ser Val Thr Ile Asp Ala				
	50	55	60	
aac ctg gcc acg gac ccg cgg ttc ctc atc ctc ctg ggt tct cca aag				299
Asn Leu Ala Thr Asp Pro Arg Phe Leu Ile Leu Leu Gly Ser Pro Lys				
	65	70	75	
ctt cgt acc ttg gcc aga ggc ttg tct cct gcg tac ctg agg ttt ggt				347
Leu Arg Thr Leu Ala Arg Gly Leu Ser Pro Ala Tyr Leu Arg Phe Gly				
80	85	90	95	
ggc acc aag aca gac ttc cta att ttc gat ccc aag aag gaa tca acc				395
Gly Thr Lys Thr Asp Phe Leu Ile Phe Asp Pro Lys Lys Glu Ser Thr				
	100	105	110	
ttt gaa gag aga agt tac tgg caa tct caa gtc aac cag gat att tgc				443
Phe Glu Glu Arg Ser Tyr Trp Gln Ser Gln Val Asn Gln Asp Ile Cys				
	115	120	125	
aaa tat gga tcc atc cct cct gat gtg gag gag aag tta cgg ttg gaa				491
Lys Tyr Gly Ser Ile Pro Pro Asp Val Glu Glu Lys Leu Arg Leu Glu				
	130	135	140	
tgg ccc tac cag gag caa ttg cta ctc cga gaa cac tac cag aaa aag				539
Trp Pro Tyr Gln Glu Gln Leu Leu Leu Arg Glu His Tyr Gln Lys Lys				
	145	150	155	
ttc aag aac agc acc tac tca aga agc tct gta gat gtg cta tac act				587
Phe Lys Asn Ser Thr Tyr Ser Arg Ser Ser Val Asp Val Leu Tyr Thr				
160	165	170	175	
ttt gca aac tgc tca gga ctg gac ttg atc ttt ggc cta aat gcg tta				635
Phe Ala Asn Cys Ser Gly Leu Asp Leu Ile Phe Gly Leu Asn Ala Leu				
	180	185	190	
tta aga aca gca gat ttg cag tgg aac agt tct aat gct cag ttg ctc				683
Leu Arg Thr Ala Asp Leu Gln Trp Asn Ser Ser Asn Ala Gln Leu Leu				
	195	200	205	
ctg gac tac tgc tct tcc aag ggg tat aac att tct tgg gaa cta ggc				731
Leu Asp Tyr Cys Ser Ser Lys Gly Tyr Asn Ile Ser Trp Glu Leu Gly				
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Asn Glu Pro Asn Ser Phe Leu Lys Lys Ala Asp Ile Phe Ile Asn Gly				
	225	230	235	

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Ser	Gln	Leu	Gly	Glu	Asp	Tyr	Ile	Gln	Leu	His	Lys	Leu	Leu	Arg	Lys	
240					245					250					255	
tcc	acc	ttc	aaa	aat	gca	aaa	ctc	tat	ggg	cct	gat	gtt	ggg	cag	cct	875
Ser	Thr	Phe	Lys	Asn	Ala	Lys	Leu	Tyr	Gly	Pro	Asp	Val	Gly	Gln	Pro	
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cga	aga	aag	acg	gct	aag	atg	ctg	aag	agc	ttc	ctg	aag	gct	ggg	gga	923
Arg	Arg	Lys	Thr	Ala	Lys	Met	Leu	Lys	Ser	Phe	Leu	Lys	Ala	Gly	Gly	
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gaa	gtg	att	gat	tca	gtt	aca	tgg	cat	cac	tac	tat	ttg	aat	gga	cgg	971
Glu	Val	Ile	Asp	Ser	Val	Thr	Trp	His	His	Tyr	Tyr	Leu	Asn	Gly	Arg	
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Thr	Ala	Thr	Arg	Glu	Asp	Phe	Leu	Asn	Pro	Asp	Val	Leu	Asp	Ile	Phe	
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Ile	Ser	Ser	Val	Gln	Lys	Val	Phe	Gln	Val	Val	Glu	Ser	Thr	Arg	Pro	
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Thr	Lys	Val	Leu	Met	Ala	Ser	Val	Gln	Gly	Ser	Lys	Arg	Arg	Lys	Leu	
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